

PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,237A

DATE: 10/03/2001

TIME: 08:24:49

Input Set : A:\3477.89 Sequence Listing.txt

Output Set: N:\CRF3\10032001\I674237A.raw

ENTERED

p.5

3 <110> APPLICANT: Egan, Sean E.  
 4 Wang, Wei  
 5 Sengar, Ameet  
 7 <120> TITLE OF INVENTION: ESE GENES AND PROTEINS  
 9 <130> FILE REFERENCE: 3477.89  
 11 <140> CURRENT APPLICATION NUMBER: US 09/674,237A  
 12 <141> CURRENT FILING DATE: 1999-04-27  
 14 <150> PRIOR APPLICATION NUMBER: PCT/CA99/00375  
 15 <151> PRIOR FILING DATE: 1999-04-27  
 17 <150> PRIOR APPLICATION NUMBER: US 60/118,739  
 18 <151> PRIOR FILING DATE: 1999-02-05  
 20 <150> PRIOR APPLICATION NUMBER: CA 2230201  
 21 <151> PRIOR FILING DATE: 1998-04-27  
 23 <160> NUMBER OF SEQ ID NOS: 33  
 25 <170> SOFTWARE: PatentIn version 3.1  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 5084  
 29 <212> TYPE: DNA  
 30 <213> ORGANISM: Mus musculus  
 32 <400> SEQUENCE: 1  
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 37 cgggcgggga tgggtgtgccc ggctgcggac tccggttccc tccgcgggcg tgcgggctgc 180  
 39 actgatttgt gtgaggggag gccgcgcgca cccgcccggg gatgagggct cgtacagcaa 240  
 41 ggtgaacgta atagaacatc ggctcagttt cccacacatt tgggtggtag cctggatgtc 300  
 43 tgggccataa ctgtggagga aagggccaaag catgaccagc agttccttag cctgaagccg 360  
 45 atagcgggat ttattactgg tgatcaagcg aggaactttt ttttccaatc tgggttacct 420  
 47 cagcctgtct tagcacaaat atgggcgcta gcggaatga ataacgatgg aaggatggat 480  
 49 caagtggat tttccatagc catgaagctt atcaaatga agctacaagg atatcagctc 540  
 51 cctccacac tttccctgt catgaaacag caaccagtgg ctatttccag tgcaccagca 600  
 53 tttggtatag gagggattgc tagcatgcca ccactcacag ctgttgctcc tgtgccaatg 660  
 55 ggctccattc cagttgttgg aatgtctcca ccttagtat cttctgtccc tccagcagca 720  
 57 gtgcctcccc tggctaacgg ggctcctccc gtcatacagc ctctgcctgc gtttgcgcat 780  
 59 cctgcagcca catggccaaa gagttcttcc ttcagcagat ctggtccagg gtcacaatta 840  
 61 aacactaagt tacagaaggc acaatcattc gatgtcgcca ggcgccctcc agcagcagaa 900  
 63 tgggctgtgc ctacgtcatc aaggctgaaa tacaggcagt tattcaacag ccacgacaaa 960  
 65 actatgagtg gacacttaac aggtccccag gcaagaacta ttctcatgca atcaagttaa 1020  
 67 cccagggctc agctggcttc aatatggaat ctttctgaca ttgatcaaga tggaaaactc 1080  
 69 actgcagaag aatttatcct agctatgcac ctaattgatg ttgcatgtc tggtcagcca 1140  
 71 ctgccgcccg tctgtcctcc agaatacatc cctccttcc tccagaagag tgcctccggc 1200  
 73 agtgggatgt ccgtcataag ctcttcttct gtggatcaga ggctgcctga ggagccgtcg 1260  
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89	aagactctgg	agtttgagtt	agaagctctg	aatgacaaaa	agcatcagct	agaaggaaaa	1740
91	cttcaggata	tcagggtgctg	actggcaacc	cagaggcaag	aaattgagag	cacgaacaag	1800
93	tctagagagc	taagaattgc	tgaaatcacc	cacttacagc	agcagttgca	ggaatctcag	1860
95	caaagtcttg	gaagacttat	tccagagaaa	cagatactca	gtgaccagtt	aaaacaagtc	1920
97	cagcagaaca	gtttgcatag	agactcgttt	cttaccctca	aaagagcctt	ggaagcaaag	1980
99	gagctggccc	ggcagcagct	cgggagcag	ctggacgagg	tggagagaga	gaccagggtca	2040
101	aagctgcagg	agattgatgt	tttcaacaac	cagctgaagg	aactgagaga	gatacatagc	2100
103	aaacagcaac	tccagaagca	gaggtccctg	gaggcagcgc	gactgaagca	gaaagagcag	2160
105	gagaggaaga	gcctggagtt	agagaagcaa	aaggaagacg	ctcagagacg	agttcaggaa	2220
107	agggacaagc	aatggctgga	gcatgtgcag	caggaggagc	agccacgccc	ccggaaaccc	2280
109	cacgaggagg	acagactgaa	gaggaagac	agtgtcagga	agaaggaggc	ggaagagaga	2340
111	gccaagccgg	aaatgcaaga	caagcagagt	cggcttttcc	atccgcatca	ggagccagct	2400
113	aagctggcca	cccaggcacc	ctgggtctacc	acagagaaag	gcccgtttac	cattttctgca	2460
115	caggagagt	taaaagtgg	atattaccga	gcgtgttacc	cctttgaatc	cagaagtcac	2520
117	gatgagatca	ccatccagcc	aggagatata	gtcatgggtg	atgaaagcca	gactggagag	2580
119	ccaggatggc	ttggaggaga	gctgaaagg	aagacgggat	ggttccctgc	aaactatgca	2640
121	gaaaagattc	cagaaaatga	ggttcccact	ccagccaaac	cagtgaccga	tctgacatct	2700
123	gccccctgcc	ccaaactggc	tctgcgtgag	acccctgctc	ctttgccagt	gacctcttct	2760
125	gagccctcca	caacccccaa	caactgggca	gacttcagtt	ccacgtggcc	cagcagctca	2820
127	aacgagaagc	cagaaacgga	caactgggat	acgtggggcg	ctcagccttc	tctgaccgta	2880
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133	tatccctgga	gagccaaaaa	agacaaccac	ttaaatttta	acaaaagtga	cgatcatcacc	3060
135	gttctggaac	agcaagacat	gtggtggttt	ggagaagttc	aaggtcagaa	gggttggttc	3120
137	cccaagtctt	acgtgaaact	catttcaggg	cccgtaaagg	aatccacaag	catcgatact	3180
139	ggccctactg	aaagtctctg	tagtctaaag	agagtggctt	ccccggccgc	caagccagcc	3240
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143	acctttcagc	aaggggatgt	gattgtggtt	accaagaaag	atggtgactg	gtggacggga	3360
145	acggtgggcg	acaagtcggg	agtcttccct	tctaactatg	tgaggcttaa	agattcagag	3420
147	ggctctggaa	ctgctgggaa	aacaggaggt	ttaggaaaaa	aacctgaaat	tgcccagggt	3480
149	attgcttctt	acgctgctac	tggctccgaa	caactcacc	tggctcctgg	gcagctgatt	3540
151	ctgatccgga	aaaagaaccc	aggtggatgg	tgggaaggag	aactgcaagc	tcgagggaaa	3600
153	aagcgccaga	taggggtggt	tccagcaaat	tatgtcaaac	ttctaagccc	cggacaacagc	3660
155	aaaatcacc	caactgagct	acccaagacc	gcagtgcagc	cagcagtgtg	ccagggtgatc	3720
157	gggatgtacg	attacaccgc	ccagaacgat	gacgaactag	ccttcagcaa	aggccagatc	3780
159	atcaacgtcc	tcaacaagga	ggacccggac	tgggtgaaag	gagaagtcag	tgggcaagtt	3840
161	gggtcttctc	catccaatta	tgtaaagctg	accacagaca	tggaccccag	ccagcaatga	3900
163	atcatatggt	gtccatcccc	ccctcaggct	tgaagtcctt	caaagagacc	cactatccca	3960
165	tatcactgcc	cagagggatg	atgggagatg	cagccttgat	catgtgactt	gcagcatgat	4020
167	cacctactgc	cttctgagta	gaagaactca	ctgcagagca	gtttacctca	tttgacctta	4080
169	gttgcatgtg	atcgaaatgt	ctgagtcact	gcgtgcagag	gcagaagcaa	attgcagaac	4140
171	tgacacagg	ggtgggtcct	tttggggctt	tcctagtcac	tcagactgac	cggccccgcc	4200
173	ttcacacggg	cgttttcaat	agtttttaaga	ttatttttaa	atgtgtattt	tagcctttta	4260
175	ataaaaaatct	caatcaatta	cttcttttgc	tatttttggt	ttacaaaaac	acccactatc	4320
177	aaggagtgcc	tgtctgcgga	cgattaaaat	gctgttccgg	gcgtaccgta	aactgagagc	4380
179	ttgctgtacc	tttgccgttt	gtccagtgtt	cccaaccaca	ttgtgtagtt	tggggctgtt	4440
181	ccctgcgta	gagcacagag	gagatgggtg	tacctgtttt	gaaaatgtgt	atgtagactg	4500
183	agcctgacta	tggaaggggt	tatgcttgtc	tgtgaccatc	acgtgtacct	gtcgcgcag	4560

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185 taccatctgt accgaagaag tagctcttcc tccatggcta aaccaccac cgtgtacagt 4620
187 gctctcatct actgcattca ttttactttg cacagtgacc ttgtagccac ctgaggaagc 4680
189 acccatggtt ccgtttggtc tcagatgtac ctagttgtgc ccggtgtttg tttttatttt 4740
191 tcaatctggc atgtcttcac accataaact agtaagaagc caactgcca ggcggttacg 4800
193 atcatcagta cccaccgtct tagtctctgt taagtgaagt ttattccagt tgctttttat 4860
195 ggaatatctt gaacaagtaa ttttcttgac aagaaagaat gtatagaagt ctccctgcaa 4920
197 ttaatttccc agtgtttaca ttttttaact agactgtggg ggttgctaca gattaatatg 4980
199 aaatggcgct cctgggtccgt gtgtgtgtta acttgtgctg tagctgaagc cgtgtgtcct 5040
201 tagatattag ttggaagtcg ggaagagaat tcgatatcaa gctt 5084
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205 <211> LENGTH: 3642
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210 <221> NAME/KEY: CDS
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212 <223> OTHER INFORMATION: Mouse Esel
215 <400> SEQUENCE: 2
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218 1 5 10 15
220 ata act gtg gag gaa agg gcc aag cat gac cag cag ttc ctt agc ctg 96
221 Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe Leu Ser Leu
222 20 25 30
224 aag ccg ata gcg gga ttt att act ggt gat caa gcg agg aac ttt ttt 144
225 Lys Pro Ile Ala Gly Phe Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe
226 35 40 45
228 ttc caa tct ggg tta cct cag cct gtc tta gca caa ata tgg gcg cta 192
229 Phe Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu
230 50 55 60
232 gcg gac atg aat aac gat gga agg atg gat caa gtg gaa ttt tcc ata 240
233 Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Val Glu Phe Ser Ile
234 65 70 75 80
236 gcc atg aag ctt atc aaa ctg aag cta caa gga tat cag ctc ccc tcc 288
237 Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Tyr Gln Leu Pro Ser
238 85 90 95
240 aca ctt ccc cct gtc atg aaa cag caa cca gtg gct att tcc agt gca 336
241 Thr Leu Pro Pro Val Met Lys Gln Gln Pro Val Ala Ile Ser Ser Ala
242 100 105 110
244 cca gca ttt ggt ata gga ggg att gct agc atg cca cca ctc aca gct 384
245 Pro Ala Phe Gly Ile Gly Gly Ile Ala Ser Met Pro Pro Leu Thr Ala
246 115 120 125
248 gtt gct cct gtg cca atg ggc tcc att cca gtt gtt gga atg tct cca 432
249 Val Ala Pro Val Pro Met Gly Ser Ile Pro Val Val Gly Met Ser Pro
250 130 135 140
252 ccc tta gta tct tct gtc cct cca gca gca gtg cct ccc ctg gct aac 480
253 Pro Leu Val Ser Ser Val Pro Pro Ala Ala Val Pro Pro Leu Ala Asn
254 145 150 155 160
256 ggg gct cct ccc gtc ata cag cct ctg cct gcg ttt gcg cat cct gca 528

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257	Gly	Ala	Pro	Pro	Val	Ile	Gln	Pro	Leu	Pro	Ala	Phe	Ala	His	Pro	Ala	
258					165				170					175			
260	gcc	aca	tgg	cca	aag	agt	tct	tcc	ttc	agc	aga	tct	ggt	cca	ggg	tca	576
261	Ala	Thr	Trp	Pro	Lys	Ser	Ser	Ser	Phe	Ser	Arg	Ser	Gly	Pro	Gly	Ser	
262				180					185					190			
264	caa	tta	aac	act	aag	tta	cag	aag	gca	caa	tca	ttc	gat	gtc	gcc	agc	624
265	Gln	Leu	Asn	Thr	Lys	Leu	Gln	Lys	Ala	Gln	Ser	Phe	Asp	Val	Ala	Ser	
266			195					200					205				
268	gcc	cct	cca	gca	gca	gaa	tgg	gct	gtg	cct	cag	tca	tca	agg	ctg	aaa	672
269	Ala	Pro	Pro	Ala	Ala	Glu	Trp	Ala	Val	Pro	Gln	Ser	Ser	Arg	Leu	Lys	
270		210					215					220					
272	tac	agg	cag	tta	ttc	aac	agc	cac	gac	aaa	act	atg	agt	gga	cac	tta	720
273	Tyr	Arg	Gln	Leu	Phe	Asn	Ser	His	Asp	Lys	Thr	Met	Ser	Gly	His	Leu	
274	225				230					235					240		
276	aca	ggt	ccc	cag	gca	aga	act	att	ctc	atg	caa	tca	agt	tta	ccc	cag	768
277	Thr	Gly	Pro	Gln	Ala	Arg	Thr	Ile	Leu	Met	Gln	Ser	Ser	Leu	Pro	Gln	
278				245					250					255			
280	gct	cag	ctg	gct	tca	ata	tgg	aat	ctt	tct	gac	att	gat	caa	gat	gga	816
281	Ala	Gln	Leu	Ala	Ser	Ile	Trp	Asn	Leu	Ser	Asp	Ile	Asp	Gln	Asp	Gly	
282				260					265					270			
284	aaa	ctc	act	gca	gaa	gaa	ttt	atc	cta	gct	atg	cac	cta	att	gat	gtt	864
285	Lys	Leu	Thr	Ala	Glu	Glu	Phe	Ile	Leu	Ala	Met	His	Leu	Ile	Asp	Val	
286			275					280					285				
288	gcc	atg	tct	ggt	cag	cca	ctg	ccg	ccc	gtc	ctg	cct	cca	gaa	tac	atc	912
289	Ala	Met	Ser	Gly	Gln	Pro	Leu	Pro	Pro	Val	Leu	Pro	Pro	Glu	Tyr	Ile	
290		290					295					300					
292	cct	cct	tcc	ttc	aga	aga	gtt	cgc	tcc	ggc	agt	ggg	atg	tcc	gtc	ata	960
293	Pro	Pro	Ser	Phe	Arg	Arg	Val	Arg	Ser	Gly	Ser	Gly	Met	Ser	Val	Ile	
294	305					310				315					320		
296	agc	tct	tct	tct	gtg	gat	cag	agg	ctg	cct	gag	gag	ccg	tcg	tca	gag	1008
297	Ser	Ser	Ser	Ser	Val	Asp	Gln	Arg	Leu	Pro	Glu	Glu	Pro	Ser	Ser	Glu	
298				325					330					335			
300	gat	gag	cag	cag	cca	gag	aag	aaa	ctg	cct	gtg	aca	ttt	gaa	gat	aag	1056
301	Asp	Glu	Gln	Gln	Pro	Glu	Lys	Lys	Leu	Pro	Val	Thr	Phe	Glu	Asp	Lys	
302				340					345					350			
304	aag	cgg	gag	aac	ttc	gag	cga	ggc	agt	gtg	gag	ctg	gag	aag	cgc	cgc	1104
305	Lys	Arg	Glu	Asn	Phe	Glu	Arg	Gly	Ser	Val	Glu	Leu	Glu	Lys	Arg	Arg	
306			355					360					365				
308	caa	gcg	ctc	ttg	gag	cag	cag	cgc	aaa	gag	cag	gag	cgg	ttg	gct	cag	1152
309	Gln	Ala	Leu	Leu	Glu	Gln	Gln	Arg	Lys	Glu	Gln	Glu	Arg	Leu	Ala	Gln	
310		370					375					380					
312	ctg	gag	cgc	gcc	gag	cag	gag	agg	aaa	gag	cgg	gag	cgc	cag	gag	cag	1200
313	Leu	Glu	Arg	Ala	Glu	Gln	Glu	Arg	Lys	Glu	Arg	Glu	Arg	Gln	Glu	Gln	
314	385					390				395					400		
316	gag	gcc	aag	cgg	cag	ctg	gag	ctg	gag	aag	cag	ctg	gag	aag	cag	cgg	1248
317	Glu	Ala	Lys	Arg	Gln	Leu	Glu	Leu	Glu	Lys	Gln	Leu	Glu	Lys	Gln	Arg	
318				405					410					415			
320	gag	ctg	gag	cgg	cag	cga	gag	gag	gag	agg	agg	aag	gag	atc	gag	agg	1296
321	Glu	Leu	Glu	Arg	Gln	Arg	Glu	Glu	Glu	Arg	Arg	Lys	Glu	Ile	Glu	Arg	

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322	420	425	430	
324	cgc gag gcc gca aaa cgg gaa ctg gaa agg cag cga caa ctt gaa tgg			1344
325	Arg Glu Ala Ala Lys Arg Glu Leu Glu Arg Gln Arg Gln Leu Glu Trp			
326	435	440	445	
328	gaa cgg aac cgg aga cag gaa ctc ctg aat cag agg aac aag gag cag			1392
329	Glu Arg Asn Arg Arg Gln Glu Leu Leu Asn Gln Arg Asn Lys Glu Gln			
330	450	455	460	
332	gag ggc acc gtg gtc ctg aag gca agg agg aag act ctg gag ttt gag			1440
333	Glu Gly Thr Val Val Leu Lys Ala Arg Arg Lys Thr Leu Glu Phe Glu			
334	465	470	475	480
336	tta gaa gct ctg aat gac aaa aag cat cag cta gaa gga aaa ctt cag			1488
337	Leu Glu Ala Leu Asn Asp Lys Lys His Gln Leu Glu Gly Lys Leu Gln			
338	485	490	495	
340	gat atc agg tgt cga ctg gca acc cag agg caa gaa att gag agc acg			1536
341	Asp Ile Arg Cys Arg Leu Ala Thr Gln Arg Gln Glu Ile Glu Ser Thr			
342	500	505	510	
344	aac aag tct aga gag cta aga att gct gaa atc acc cac tta cag cag			1584
345	Asn Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln Gln			
346	515	520	525	
348	cag ttg cag gaa tct cag caa atg ctt gga aga ctt att cca gag aaa			1632
349	Gln Leu Gln Glu Ser Gln Gln Met Leu Gly Arg Leu Ile Pro Glu Lys			
350	530	535	540	
352	cag ata ctc agt gac cag tta aaa caa gtc cag cag aac agt ttg cat			1680
353	Gln Ile Leu Ser Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu His			
354	545	550	555	560
356	aga gac tcg ctt ctt acc ctc aaa aga gcc ttg gaa gca aag gag ctg			1728
357	Arg Asp Ser Leu Leu Thr Leu Lys Arg Ala Leu Glu Ala Lys Glu Leu			
358	565	570	575	
360	gcc cgg cag cag ctc cgg gag cag ctg gac gag gtg gag aga gag acc			1776
361	Ala Arg Gln Gln Leu Arg Glu Gln Leu Asp Glu Val Glu Arg Glu Thr			
362	580	585	590	
364	agg tca aag ctg cag gag att gat gtt ttc aac aac cag ctg aag gaa			1824
365	Arg Ser Lys Leu Gln Glu Ile Asp Val Phe Asn Asn Gln Leu Lys Glu			
366	595	600	605	
368	ctg aga gag ata cat agc aaa cag caa ctc cag aag cag agg tcc ctg			1872
369	Leu Arg Glu Ile His Ser Lys Gln Gln Leu Gln Lys Gln Arg Ser Leu			
370	610	615	620	
372	gag gca gcg cga ctg aag cag aaa gag cag gag agg aag agc ctg gag			1920
373	Glu Ala Ala Arg Leu Lys Gln Lys Glu Gln Glu Arg Lys Ser Leu Glu			
374	625	630	635	640
376	tta gag aag caa aag gaa gac gct cag aga cga gtt cag gaa agg gac			1968
377	Leu Glu Lys Gln Lys Glu Asp Ala Gln Arg Arg Val Gln Glu Arg Asp			
378	645	650	655	
380	aag caa tgg ctg gag cat gtg cag cag gag gag cag cca cgc ccc cgg			2016
381	Lys Gln Trp Leu Glu His Val Gln Gln Glu Glu Gln Pro Arg Pro Arg			
382	660	665	670	
384	aaa ccc cac gag gag gac aga ctg aag agg gaa gac agt gtc agg aag			2064
385	Lys Pro His Glu Glu Asp Arg Leu Lys Arg Glu Asp Ser Val Arg Lys			
386	675	680	685	

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\3477.89 Sequence Listing.txt

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L:2218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18